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SEQUENCE LISTING

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HUDAK, KATALIN A.

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<130> OCIRS 3.3-072

<140> 09/869,176

<141> 2001-06-26

<150> 60/115,791

<151> 1998-12-31

<150> PCT/US99/31312

<151> 1999-12-30

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cat ttg gct gaa atc caa ttg aac ggt ggt tcc atc tct gaa aag gtt	576
His Leu Ala Glu Ile Gln Leu Asn Gly Gly Ser Ile Ser Glu Lys Val	
180 185 190	
gac tgg gct cgt gaa cat ttc gaa aag act gtt gct gtc gac agc gtt	624
Asp Trp Ala Arg Glu His Phe Glu Lys Thr Val Ala Val Asp Ser Val	
195 200 205	
ttt gaa caa aac gaa atg att gac gct att gct gtc acc aag ggt cac	672
Phe Glu Gln Asn Glu Met Ile Asp Ala Ile Ala Val Thr Lys Gly His	
210 215 220	
ggt ttc gaa ggt gtt acc cac aga tgg ggt act aag aaa ttg cca aga	720
Gly Phe Glu Gly Val Thr His Arg Trp Gly Thr Lys Lys Leu Pro Arg	
225 230 235 240	
aag act cac aga ggt cta aga aag gtt gct tgt att ggt gct tgc cat	768
Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly Ala Cys His	
245 250 255	

cca gcc cac gtt atg tgg agt gtt gcc aga gct ggt caa aga ggt tac 816
 Pro Ala His Val Met Trp Ser Val Ala Arg Ala Gly Gln Arg Gly Tyr
 260 265 270

cat tcc aga acc tcc att aac cac aag att tac aga gtc ggt aag ggt 864
 His Ser Arg Thr Ser Ile Asn His Lys Ile Tyr Arg Val Gly Lys Gly
 275 280 285

gat gat gaa gct aac ggt gct acc agc ttc gac aga acc aag aag act 912
 Asp Asp Glu Ala Asn Gly Ala Thr Ser Phe Asp Arg Thr Lys Lys Thr
 290 295 300

att acc cca atg ggt ggt ttc gtc cac tac ggt gaa att aag aac gac 960
 Ile Thr Pro Met Gly Gly Phe Val His Tyr Gly Glu Ile Lys Asn Asp
 305 310 315 320

ttc atc atg gtt aaa ggt tgt atc cca ggt aac aga aag aga att gtt 1008
 Phe Ile Met Val Lys Gly Cys Ile Pro Gly Asn Arg Lys Arg Ile Val
 325 330 335

act ttg aga aag tct ttg tac acc aac act tct aga aag gct ttg gaa 1056
 Thr Leu Arg Lys Ser Leu Tyr Thr Asn Thr Ser Arg Lys Ala Leu Glu
 340 345 350

gaa gtc agc ttg aag tgg att gac act gct tct aag ttc ggt aag ggt 1104
 Glu Val Ser Leu Lys Trp Ile Asp Thr Ala Ser Lys Phe Gly Lys Gly
 355 360 365

aga ttc caa acc cca gct gaa aag cat gct ttc atg ggt act ttg aag 1152
 Arg Phe Gln Thr Pro Ala Glu Lys His Ala Phe Met Gly Thr Leu Lys
 370 375 380

aag gac ttg taa 1164
 Lys Asp Leu
 385

<210> 8
 <211> 387
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 8
 Met Ser His Arg Lys Tyr Glu Ala Pro Arg His Gly His Leu Gly Phe
 1 5 10 15

Leu Pro Arg Lys Arg Ala Ala Ser Ile Arg Ala Arg Val Lys Ala Phe
 20 25 30

Pro Lys Asp Asp Arg Ser Lys Pro Val Ala Leu Thr Ser Phe Leu Gly
 35 40 45

Tyr Lys Ala Gly Met Thr Thr Ile Val Arg Asp Leu Asp Arg Pro Gly
 50 55 60

Ser Lys Phe His Lys Arg Glu Val Val Glu Ala Val Thr Val Val Asp
 65 70 75 80

Thr	Pro	Pro	Val	Val	Val	Val	Gly	Val	Val	Gly	Tyr	Val	Glu	Thr	Pro	85	90	95
Arg	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Val	Trp	Ala	Glu	His	Leu	Ser	Asp	100	105	110
Glu	Val	Lys	Arg	Arg	Phe	Tyr	Lys	Asn	Trp	Tyr	Lys	Ser	Lys	Lys	Lys	115	120	125
Ala	Phe	Thr	Lys	Tyr	Ser	Ala	Lys	Tyr	Ala	Gln	Asp	Gly	Ala	Gly	Ile	130	135	140
Glu	Arg	Glu	Leu	Ala	Arg	Ile	Lys	Lys	Tyr	Ala	Ser	Val	Val	Arg	Val	145	150	155
Leu	Val	His	Thr	Gln	Ile	Arg	Lys	Thr	Pro	Leu	Ala	Gln	Lys	Lys	Ala	165	170	175
His	Leu	Ala	Glu	Ile	Gln	Leu	Asn	Gly	Gly	Ser	Ile	Ser	Glu	Lys	Val	180	185	190
Asp	Trp	Ala	Arg	Glu	His	Phe	Glu	Lys	Thr	Val	Ala	Val	Asp	Ser	Val	195	200	205
Phe	Glu	Gln	Asn	Glu	Met	Ile	Asp	Ala	Ile	Ala	Val	Thr	Lys	Gly	His	210	215	220
Gly	Phe	Glu	Gly	Val	Thr	His	Arg	Trp	Gly	Thr	Lys	Lys	Leu	Pro	Arg	225	230	235
Lys	Thr	His	Arg	Gly	Leu	Arg	Lys	Val	Ala	Cys	Ile	Gly	Ala	Cys	His	245	250	255
Pro	Ala	His	Val	Met	Trp	Ser	Val	Ala	Arg	Ala	Gly	Gln	Arg	Gly	Tyr	260	265	270
His	Ser	Arg	Thr	Ser	Ile	Asn	His	Lys	Ile	Tyr	Arg	Val	Gly	Lys	Gly	275	280	285
Asp	Asp	Glu	Ala	Asn	Gly	Ala	Thr	Ser	Phe	Asp	Arg	Thr	Lys	Lys	Thr	290	295	300
Ile	Thr	Pro	Met	Gly	Gly	Phe	Val	His	Tyr	Gly	Glu	Ile	Lys	Asn	Asp	305	310	315
Phe	Ile	Met	Val	Lys	Gly	Cys	Ile	Pro	Gly	Asn	Arg	Lys	Arg	Ile	Val	325	330	335
Thr	Leu	Arg	Lys	Ser	Leu	Tyr	Thr	Asn	Thr	Ser	Arg	Lys	Ala	Leu	Glu	340	345	350
Glu	Val	Ser	Leu	Lys	Trp	Ile	Asp	Thr	Ala	Ser	Lys	Phe	Gly	Lys	Gly	355	360	365
Arg	Phe	Gln	Thr	Pro	Ala	Glu	Lys	His	Ala	Phe	Met	Gly	Thr	Leu	Lys	370	375	380

Lys Asp Leu
385

<210> 9
<211> 1164
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (1)..(1161)

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Met Ser His Arg Lys Tyr Glu Ala Pro Arg His Gly His Leu Gly Phe
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ttg cca aga aag aga gct gcc tcc atc aga gct aga gtt aag gct ttt 96
Leu Pro Arg Lys Arg Ala Ala Ser Ile Arg Ala Arg Val Lys Ala Phe
              20              25              30

cca aag gat gac aga tcc aag cca gtt gct cta act tcc ttc ttg ggt 144
Pro Lys Asp Asp Arg Ser Lys Pro Val Ala Leu Thr Ser Phe Leu Gly
              35              40              45

tac aag gct ggt atg acc acc att gtc aga gat ttg gac aga cca ggt 192
Tyr Lys Ala Gly Met Thr Thr Ile Val Arg Asp Leu Asp Arg Pro Gly
              50              55              60

tct aag ttc cac aag cgt gaa gtt gtc gaa gct gtc acc gtt gtt gac 240
Ser Lys Phe His Lys Arg Glu Val Val Glu Ala Val Thr Val Val Asp
  65              70              75              80

act cca cca gtt gtc gtt gtt ggt gtt gtc ggt tac gtc gaa acc cca 288
Thr Pro Pro Val Val Val Val Gly Val Val Gly Tyr Val Glu Thr Pro
              85              90              95

aga ggt ttg aga tct ttg acc acc gtc tgg gct gaa cat ttg tct gac 336
Arg Gly Leu Arg Ser Leu Thr Thr Val Trp Ala Glu His Leu Ser Asp
              100              105              110

gaa gtc aag aga aga ttc tac aag aac tgg tac aag tct aag aag aag 384
Glu Val Lys Arg Arg Phe Tyr Lys Asn Trp Tyr Lys Ser Lys Lys Lys
              115              120              125

gct ttc acc aaa tac tct gcc aag tac gct caa gat ggt gct ggt att 432
Ala Phe Thr Lys Tyr Ser Ala Lys Tyr Ala Gln Asp Gly Ala Gly Ile
              130              135              140

gaa aga gaa ttg gct aga atc aag aag tac gct tcc gtc gtc aga gtt 480
Glu Arg Glu Leu Ala Arg Ile Lys Lys Tyr Ala Ser Val Val Arg Val
  145              150              155              160

ttg gtc cac act caa atc aga aag act cca ttg gct caa aag aag gct 528
Leu Val His Thr Gln Ile Arg Lys Thr Pro Leu Ala Gln Lys Lys Ala
              165              170              175

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cat ttg gct gaa atc caa ttg aac ggt ggt tcc atc tct gaa aag gtt	576
His Leu Ala Glu Ile Gln Leu Asn Gly Gly Ser Ile Ser Glu Lys Val	
180 185 190	
gac tgg gct cgt gaa cat ttc gaa aag act gtt gct gtc gac agc gtt	624
Asp Trp Ala Arg Glu His Phe Glu Lys Thr Val Ala Val Asp Ser Val	
195 200 205	
ttt gaa caa aac gaa atg att gac gct att gct gtc acc aag ggt cac	672
Phe Glu Gln Asn Glu Met Ile Asp Ala Ile Ala Val Thr Lys Gly His	
210 215 220	
ggg ttc gaa ggt gtt acc cac aga tgg ggt act aag aaa ttg cca aga	720
Gly Phe Glu Gly Val Thr His Arg Trp Gly Thr Lys Lys Leu Pro Arg	
225 230 235 240	
aag act cac aga ggt cta aga aag gtt gct tgt att ggt gct tgc cat	768
Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly Ala Cys His	
245 250 255	
tca gcc cac gtt atg tgg agt gtt gcc aga gct ggt caa aga ggt tac	816
Ser Ala His Val Met Trp Ser Val Ala Arg Ala Gly Gln Arg Gly Tyr	
260 265 270	
cat tcc aga acc tcc att aac cac aag att tac aga gtc ggt aag ggt	864
His Ser Arg Thr Ser Ile Asn His Lys Ile Tyr Arg Val Gly Lys Gly	
275 280 285	
gat gat gaa gct aac ggt gct acc agc ttc gac aga acc aag aag act	912
Asp Asp Glu Ala Asn Gly Ala Thr Ser Phe Asp Arg Thr Lys Lys Thr	
290 295 300	
att acc cca atg ggt ggt ttc gtc cac tac ggt gaa att aag aac gac	960
Ile Thr Pro Met Gly Gly Phe Val His Tyr Gly Glu Ile Lys Asn Asp	
305 310 315 320	
ttc atc atg gtt aaa ggt tgt atc cca ggt aac aga aag aga att gtt	1008
Phe Ile Met Val Lys Gly Cys Ile Pro Gly Asn Arg Lys Arg Ile Val	
325 330 335	
act ttg aga aag tct ttg tac acc aac act tct aga aag gct ttg gaa	1056
Thr Leu Arg Lys Ser Leu Tyr Thr Asn Thr Ser Arg Lys Ala Leu Glu	
340 345 350	
gaa gtc agc ttg aag tgg att gac act gct tct aag ttc ggt aag ggt	1104
Glu Val Ser Leu Lys Trp Ile Asp Thr Ala Ser Lys Phe Gly Lys Gly	
355 360 365	
aga ttc caa acc cca gct gaa aag cat gct ttc atg ggt act ttg aag	1152
Arg Phe Gln Thr Pro Ala Glu Lys His Ala Phe Met Gly Thr Leu Lys	
370 375 380	
aag gac ttg taa	1164
Lys Asp Leu	
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<210> 10
 <211> 387
 <212> PRT
 <213> *Saccharomyces cerevisiae*

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 20 25 30
 Pro Lys Asp Asp Arg Ser Lys Pro Val Ala Leu Thr Ser Phe Leu Gly
 35 40 45
 Tyr Lys Ala Gly Met Thr Thr Ile Val Arg Asp Leu Asp Arg Pro Gly
 50 55 60
 Ser Lys Phe His Lys Arg Glu Val Val Glu Ala Val Thr Val Val Asp
 65 70 75 80
 Thr Pro Pro Val Val Val Val Gly Val Val Gly Tyr Val Glu Thr Pro
 85 90 95
 Arg Gly Leu Arg Ser Leu Thr Thr Val Trp Ala Glu His Leu Ser Asp
 100 105 110
 Glu Val Lys Arg Arg Phe Tyr Lys Asn Trp Tyr Lys Ser Lys Lys Lys
 115 120 125
 Ala Phe Thr Lys Tyr Ser Ala Lys Tyr Ala Gln Asp Gly Ala Gly Ile
 130 135 140
 Glu Arg Glu Leu Ala Arg Ile Lys Lys Tyr Ala Ser Val Val Arg Val
 145 150 155 160
 Leu Val His Thr Gln Ile Arg Lys Thr Pro Leu Ala Gln Lys Lys Ala
 165 170 175
 His Leu Ala Glu Ile Gln Leu Asn Gly Gly Ser Ile Ser Glu Lys Val
 180 185 190
 Asp Trp Ala Arg Glu His Phe Glu Lys Thr Val Ala Val Asp Ser Val
 195 200 205
 Phe Glu Gln Asn Glu Met Ile Asp Ala Ile Ala Val Thr Lys Gly His
 210 215 220
 Gly Phe Glu Gly Val Thr His Arg Trp Gly Thr Lys Lys Leu Pro Arg
 225 230 235 240
 Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly Ala Cys His
 245 250 255
 Ser Ala His Val Met Trp Ser Val Ala Arg Ala Gly Gln Arg Gly Tyr
 260 265 270

His Ser Arg Thr Ser Ile Asn His Lys Ile Tyr Arg Val Gly Lys Gly
 275 280 285
 Asp Asp Glu Ala Asn Gly Ala Thr Ser Phe Asp Arg Thr Lys Lys Thr
 290 295 300
 Ile Thr Pro Met Gly Gly Phe Val His Tyr Gly Glu Ile Lys Asn Asp
 305 310 315 320
 Phe Ile Met Val Lys Gly Cys Ile Pro Gly Asn Arg Lys Arg Ile Val
 325 330 335
 Thr Leu Arg Lys Ser Leu Tyr Thr Asn Thr Ser Arg Lys Ala Leu Glu
 340 345 350
 Glu Val Ser Leu Lys Trp Ile Asp Thr Ala Ser Lys Phe Gly Lys Gly
 355 360 365
 Arg Phe Gln Thr Pro Ala Glu Lys His Ala Phe Met Gly Thr Leu Lys
 370 375 380
 Lys Asp Leu
 385

<210> 11
 <211> 1164
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1161)

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 Leu Pro Arg Lys Arg Ala Ala Ser Ile Arg Ala Arg Val Lys Ala Phe
 20 25 30
 cca aag gat gac aga tcc aag cca gtt gct cta act tcc ttc ttg ggt 144
 Pro Lys Asp Asp Arg Ser Lys Pro Val Ala Leu Thr Ser Phe Leu Gly
 35 40 45
 tac aag gct ggt atg acc acc att gtc aga gat ttg gac aga cca ggt 192
 Tyr Lys Ala Gly Met Thr Thr Ile Val Arg Asp Leu Asp Arg Pro Gly
 50 55 60
 tct aag ttc cac aag cgt gaa gtt gtc gaa gct gtc acc gtt gtt gac 240
 Ser Lys Phe His Lys Arg Glu Val Val Glu Ala Val Thr Val Val Asp
 65 70 75 80

act cca cca gtt gtc gtt gtt ggt gtt gtc ggt tac gtc gaa acc cca	288
Thr Pro Pro Val Val Val Gly Val Val Gly Tyr Val Glu Thr Pro	
85 90 95	
aga ggt ttg aga tct ttg acc acc gtc tgg gct gaa cat ttg tct gac	336
Arg Gly Leu Arg Ser Leu Thr Thr Val Trp Ala Glu His Leu Ser Asp	
100 105 110	
gaa gtc aag aga aga ttc tac aag aac tgg tac aag tct aag aag aag	384
Glu Val Lys Arg Arg Phe Tyr Lys Asn Trp Tyr Lys Ser Lys Lys Lys	
115 120 125	
gct ttc acc aaa tac tct gcc aag tac gct caa gat ggt gct ggt att	432
Ala Phe Thr Lys Tyr Ser Ala Lys Tyr Ala Gln Asp Gly Ala Gly Ile	
130 135 140	
gaa aga gaa ttg gct aga atc aag aag tac gct tcc gtc gtc aga gtt	480
Glu Arg Glu Leu Ala Arg Ile Lys Lys Tyr Ala Ser Val Val Arg Val	
145 150 155 160	
ttg gtc cac act caa atc aga aag act cca ttg gct caa aag aag gct	528
Leu Val His Thr Gln Ile Arg Lys Thr Pro Leu Ala Gln Lys Lys Ala	
165 170 175	
cat ttg gct gaa atc caa ttg aac ggt ggt tcc atc tct gaa aag gtt	576
His Leu Ala Glu Ile Gln Leu Asn Gly Gly Ser Ile Ser Glu Lys Val	
180 185 190	
gac tgg gct cgt gaa cat ttc gaa aag act gtt gct gtc gac agc gtt	624
Asp Trp Ala Arg Glu His Phe Glu Lys Thr Val Ala Val Asp Ser Val	
195 200 205	
ttt gaa caa aac gaa atg att gac gct att gct gtc acc aag ggt cac	672
Phe Glu Gln Asn Glu Met Ile Asp Ala Ile Ala Val Thr Lys Gly His	
210 215 220	
ggt ttc gaa ggt gtt acc cac aga tgg ggt act aag aaa ttg cca aga	720
Gly Phe Glu Gly Val Thr His Arg Trp Gly Thr Lys Lys Leu Pro Arg	
225 230 235 240	
aag act cac aga ggt cta aga aag gtt gct tgt att ggt gct tgg cat	768
Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly Ala Trp His	
245 250 255	
cca gcc cac gtt atg tgg agt gtt gcc aga gct ggt caa aga ggt tac	816
Pro Ala His Val Met Trp Ser Val Ala Arg Ala Gly Gln Arg Gly Tyr	
260 265 270	
cat tcc aga acc tcc att aac cac aag act tac aga gtc ggt aag ggt	864
His Ser Arg Thr Ser Ile Asn His Lys Thr Tyr Arg Val Gly Lys Gly	
275 280 285	
gat gat gaa gct aac ggt gct acc agc ttc gac aga acc aag aag act	912
Asp Asp Glu Ala Asn Gly Ala Thr Ser Phe Asp Arg Thr Lys Lys Thr	
290 295 300	

att acc cca atg ggt ggt ttc gtc cac tac ggt gaa att aag aac gac 960
 Ile Thr Pro Met Gly Gly Phe Val His Tyr Gly Glu Ile Lys Asn Asp
 305 310 315 320

 ttc atc atg gtt aaa ggt tgt atc cca ggt aac aga aag aga att gtt 1008
 Phe Ile Met Val Lys Gly Cys Ile Pro Gly Asn Arg Lys Arg Ile Val
 325 330 335

 act ttg aga aag tct ttg tac acc aac act tct aga aag gct ttg gaa 1056
 Thr Leu Arg Lys Ser Leu Tyr Thr Asn Thr Ser Arg Lys Ala Leu Glu
 340 345 350

 gaa gtc agc ttg aag tgg att gac act gct tct aag ttc ggt aag ggt 1104
 Glu Val Ser Leu Lys Trp Ile Asp Thr Ala Ser Lys Phe Gly Lys Gly
 355 360 365

 aga ttc caa acc cca gct gaa aag cat gct ttc atg ggt act ttg aag 1152
 Arg Phe Gln Thr Pro Ala Glu Lys His Ala Phe Met Gly Thr Leu Lys
 370 375 380

 aag gac ttg taa 1164
 Lys Asp Leu
 385

<210> 12
 <211> 387
 <212> PRT
 <213> *Saccharomyces cerevisiae*

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 Pro Lys Asp Asp Arg Ser Lys Pro Val Ala Leu Thr Ser Phe Leu Gly
 35 40 45

 Tyr Lys Ala Gly Met Thr Thr Ile Val Arg Asp Leu Asp Arg Pro Gly
 50 55 60

 Ser Lys Phe His Lys Arg Glu Val Val Glu Ala Val Thr Val Val Asp
 65 70 75 80

 Thr Pro Pro Val Val Val Val Gly Val Val Gly Tyr Val Glu Thr Pro
 85 90 95

 Arg Gly Leu Arg Ser Leu Thr Thr Val Trp Ala Glu His Leu Ser Asp
 100 105 110

 Glu Val Lys Arg Arg Phe Tyr Lys Asn Trp Tyr Lys Ser Lys Lys Lys
 115 120 125

 Ala Phe Thr Lys Tyr Ser Ala Lys Tyr Ala Gln Asp Gly Ala Gly Ile
 130 135 140

Glu Arg Glu Leu Ala Arg Ile Lys Lys Tyr Ala Ser Val Val Arg Val
 145 150 155 160
 Leu Val His Thr Gln Ile Arg Lys Thr Pro Leu Ala Gln Lys Lys Ala
 165 170 175
 His Leu Ala Glu Ile Gln Leu Asn Gly Gly Ser Ile Ser Glu Lys Val
 180 185 190
 Asp Trp Ala Arg Glu His Phe Glu Lys Thr Val Ala Val Asp Ser Val
 195 200 205
 Phe Glu Gln Asn Glu Met Ile Asp Ala Ile Ala Val Thr Lys Gly His
 210 215 220
 Gly Phe Glu Gly Val Thr His Arg Trp Gly Thr Lys Lys Leu Pro Arg
 225 230 235 240
 Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly Ala Trp His
 245 250 255
 Pro Ala His Val Met Trp Ser Val Ala Arg Ala Gly Gln Arg Gly Tyr
 260 265 270
 His Ser Arg Thr Ser Ile Asn His Lys Thr Tyr Arg Val Gly Lys Gly
 275 280 285
 Asp Asp Glu Ala Asn Gly Ala Thr Ser Phe Asp Arg Thr Lys Lys Thr
 290 295 300
 Ile Thr Pro Met Gly Gly Phe Val His Tyr Gly Glu Ile Lys Asn Asp
 305 310 315 320
 Phe Ile Met Val Lys Gly Cys Ile Pro Gly Asn Arg Lys Arg Ile Val
 325 330 335
 Thr Leu Arg Lys Ser Leu Tyr Thr Asn Thr Ser Arg Lys Ala Leu Glu
 340 345 350
 Glu Val Ser Leu Lys Trp Ile Asp Thr Ala Ser Lys Phe Gly Lys Gly
 355 360 365
 Arg Phe Gln Thr Pro Ala Glu Lys His Ala Phe Met Gly Thr Leu Lys
 370 375 380
 Lys Asp Leu
 385

<210> 13

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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ccccggtacc tcacgcacac tggaatgaat

30

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
ccccgagcgc aacctccatt ttggacttgg

30